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1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/597,604

DATE: 08/12/2002
TIME: 15:29:56

Input Set : A:\97-186-D.seqlist.ST25.txt
Output Set: N:\CRF4\08122002\I597604.raw

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3 <110> APPLICANT: Moskal, Joseph
4 Yamamoto, Hirotaka
6 <120> TITLE OF INVENTION: Detection and Treatment of Glyco-Enzyme-Related Disease
8 <130> FILE REFERENCE: 97,186-D
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/597,604
11 <141> CURRENT FILING DATE: 2000-06-20
13 <160> NUMBER OF SEQ ID NOS: 20
15 <170> SOFTWARE: PatentIn version 3.1
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 20
19 <212> TYPE: DNA
20 <213> ORGANISM: Artificial Sequence
22 <220> FEATURE:
23 <223> OTHER INFORMATION: alpha 2,3-ST sense primer
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32 <213> ORGANISM: Artificial Sequence
34 <220> FEATURE:
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55 <212> TYPE: DNA
56 <213> ORGANISM: Artificial Sequence
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65 <210> SEQ ID NO: 5
66 <211> LENGTH: 1128
67 <212> TYPE: DNA

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71 <221> NAME/KEY: misc_feature
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80 tcagtgggttc tttcctttga ctccgctgga caaacactag gctcagagta tgatcggttg 180
82 ggcttctctcc tgaatctgga ctctaaactg cctgctgaat tagccaccaa gtacgcaaac 240
84 ttttcagagg gagcttgcaa gcctggctat gcttcagcct tgatgacggc catcttcccc 300
86 cgggttctcca agccagcacc catgttcctg gatgactcct ttcgcaagtg ggctagaatc 360
88 cgggagttcg tgccgccttt tgggatcaaa ggtcaagaca atctgatcaa agccatcttg 420
90 tcagtcacca aagagtaccg cctgaccctt gccttggaca gcctccgctg ccgccgctgc 480
92 atcatcgtgg gcaatggagg cgttcttgcc aacaagtctc tggggtcacg aattgacgac 540
94 tatgacattg tggtagact gaattcagca ccagtgaag gctttgagaa ggacgtgggc 600
96 agcaaaacga cactgcgcac cacctacccc gagggcgcca tgcagcgcc tgagcagtag 660
98 gagcgcgatt ctctctttgt cctcgccggc ttcaagtggc aggactttaa gtggttgaaa 720
100 tacatcgtct acaaggagag agtgagtgc tccgatggct tctggaaatc tgtggccact 780
102 cgagtgcaca aggagccccc tgagattcga atcctcaacc catatttcat ccaggaggcc 840
104 gccttcaccc tcattggcct gcccttcaac aatggcctca tgggccgggg gaacatccct 900
106 acccttggca gtgtggcagt gaccatggca ctacacggct gtgacgaggt ggcagtcgca 960
108 ggatttggct atgacatgag cacacccaac gcaccctgc actactatga gaccgttcgc 1020
110 atggcagcca tcaaagagtc ctggacgcac aatatccagc gagagaaaga gtttctgcgg 1080
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131 Phe Leu Val Leu Gly Phe Leu Tyr Tyr Ser Ala Trp Lys Leu His Leu
132 20 25 30
135 Leu Gln Trp Glu Glu Asp Ser Asn Ser Val Val Leu Ser Phe Asp Ser
136 35 40 45
139 Ala Gly Gln Thr Leu Gly Ser Glu Tyr Asp Arg Leu Gly Phe Leu Leu
140 50 55 60
143 Asn Leu Asp Ser Lys Leu Pro Ala Glu Leu Ala Thr Lys Tyr Ala Asn
144 65 70 75 80
147 Phe Ser Glu Gly Ala Cys Lys Pro Gly Tyr Ala Ser Ala Leu Met Thr
148 85 90 95
151 Ala Ile Phe Pro Arg Phe Ser Lys Pro Ala Pro Met Phe Leu Asp Asp
152 100 105 110
155 Ser Phe Arg Lys Trp Ala Arg Ile Arg Glu Phe Val Pro Pro Phe Gly
156 115 120 125
159 Ile Lys Gly Gln Asp Asn Leu Ile Lys Ala Ile Leu Ser Val Thr Lys

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160      130      135      140
163 Glu Tyr Arg Leu Thr Pro Ala Leu Asp Ser Leu Arg Cys Arg Arg Cys
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167 Ile Ile Val Gly Asn Gly Gly Val Leu Ala Asn Lys Ser Leu Gly Ser
168      165      170      175
171 Arg Ile Asp Asp Tyr Asp Ile Val Val Arg Leu Asn Ser Ala Pro Val
172      180      185      190
175 Lys Gly Phe Glu Lys Asp Val Gly Ser Lys Thr Thr Leu Arg Ile Thr
176      195      200      205
179 Tyr Pro Glu Gly Ala Met Gln Arg Pro Glu Gln Tyr Glu Arg Asp Ser
180      210      215      220
183 Leu Phe Val Leu Ala Gly Phe Lys Trp Gln Asp Phe Lys Trp Leu Lys
184 225      230      235      240
187 Tyr Ile Val Tyr Lys Glu Arg Val Ser Ala Ser Asp Gly Phe Trp Lys
188      245      250      255
191 Ser Val Ala Thr Arg Val Pro Lys Glu Pro Pro Glu Ile Arg Ile Leu
192      260      265      270
195 Asn Pro Tyr Phe Ile Gln Glu Ala Ala Phe Thr Leu Ile Gly Leu Pro
196      275      280      285
199 Phe Asn Asn Gly Leu Met Gly Arg Gly Asn Ile Pro Thr Leu Gly Ser
200      290      295      300
203 Val Ala Val Thr Met Ala Leu His Gly Cys Asp Glu Val Ala Val Ala
204 305      310      315      320
207 Gly Phe Gly Tyr Asp Met Ser Thr Pro Asn Ala Pro Leu His Tyr Tyr
208      325      330      335
211 Glu Thr Val Arg Met Ala Ala Ile Lys Glu Ser Trp Thr His Asn Ile
212      340      345      350
215 Gln Arg Glu Lys Glu Phe Leu Arg Lys Leu Val Lys Ala Arg Val Ile
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219 Thr Asp Leu Ser Ser Gly Ile
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223 <210> SEQ ID NO: 7
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229 <221> NAME/KEY: misc_feature
230 <223> OTHER INFORMATION: Hex B DNA
233 <400> SEQUENCE: 7

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238 gcgctgctgt tggcgacact gctggcggcg atgttggcgc tgcgtactca ggtggcgctg 180
240 gtgggtgcagg tggcgagggc ggctcgggcc ccgagcgtct cggccaagcc ggggcccggc 240
242 ctgtggcccc tgccgtcttc ggtgaagatg accccgaacc tgctgcatct cgcggcgagg 300
244 aacttctaca tcagccacag ccccaattcc acggcgggcc cctcctgcac cctgctggag 360
246 gaagcgtttc gacgatatca tggctatatt tttggtttct acaagtggca tcatgaacct 420
248 gctgaattcc aggctaaaac ccaggttcag caacttcttg tctcaatcac ccttcagtca 480
250 gagtgtgatg ctttcccaa catatcttca gatgagtctt atactttact tgtgaaagaa 540
252 ccagtggtctg tccttaaggc caacagagtt tggggagcat tacgaggttt agagaccttt 600

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254 agccagtttag tttatcaaga ttcttatgga actttcacca tcaatgaatc caccattatt 660
256 gattctccaa ggttttctca cagaggaatt ttgattgata catccagaca ttatctgcca 720
258 gttaagatta ttcttaaaac tctggatgcc atggctttaa ataagtttaa tgttcttcac 780
260 tggcacatag ttgatgacca gtctttccca tatcagagca tcacttttcc tgagttaagc 840
262 aataaaggaa gctattcttt gtctcatgtt tatacaccaa atgatgtccg tatggtgatt 900
264 gaatatgcca gattacgagg aattcgagtc ctgccagaat ttgatacccc tgggcataca 960
266 ctatcttggg gaaaagggtca gaaagacctc ctgactccat gttacagtag acaaaacaag 1020
268 ttggactctt ttggacctat aaaccctact ctgaatacaa catacagctt ccttactaca 1080
270 tttttcaaag aaattagtga ggtgtttcca gatcaattca ttcatttggg aggagatgaa 1140
272 gtggaattta aatgttggga atcaaatcca aaaattcaag atttcatgag gcaaaaaggc 1200
274 ttgggcacag attttaagaa actagaatct ttctacattc aaaaggtttt ggatattatt 1260
276 gcaaccataa acaagggatc cattgtctgg caggagggttt ttgatgataa agcaaagctt 1320
278 gcgcccggca caatagttag agtatggaaa gacagcgcac atcctgagga actcagtaga 1380
280 gtcacagcat ctggcttccc tgtaatcctt tctgtcctt ggtacttaga tttgattagc 1440
282 tatggacaag attggaggaa atactataaa gtggaacctc ttgattttgg cggtaactcag 1500
284 aaacagaaac aacttttcat tgggtggagaa gcttgtctat ggggagaata tgtggatgca 1560
286 actaacctca ctccaagatt atggcctcgg gcaagtgtctg ttggtgagag actctggagt 1620
288 tccaaagatg tcagagatat ggatgacgcc tatgacagac tgacaaggca ccgctgcagg 1680
290 atggtcgaac gtggaatagc tgcacaacct ctttatgctg gatattgtaa ccatgagaac 1740
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304 <223> OTHER INFORMATION: HexB Polypeptide

307 <400> SEQUENCE: 8

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314 20 25 30
317 Val Ala Leu Val Val Gln Val Ala Glu Ala Ala Arg Ala Pro Ser Val
318 35 40 45
321 Ser Ala Lys Pro Gly Pro Ala Leu Trp Pro Leu Pro Leu Ser Val Lys
322 50 55 60
325 Met Thr Pro Asn Leu Leu His Leu Ala Pro Glu Asn Phe Tyr Ile Ser
326 65 70 75 80
329 His Ser Pro Asn Ser Thr Ala Gly Pro Ser Cys Thr Leu Leu Glu Glu
330 85 90 95
333 Ala Phe Arg Arg Tyr His Gly Tyr Ile Phe Gly Phe Tyr Lys Trp His
334 100 105 110
337 His Glu Pro Ala Glu Phe Gln Ala Lys Thr Gln Val Gln Gln Leu Leu
338 115 120 125
341 Val Ser Ile Thr Leu Gln Ser Glu Cys Asp Ala Phe Pro Asn Ile Ser
342 130 135 140
345 Ser Asp Glu Ser Tyr Thr Leu Leu Val Lys Glu Pro Val Ala Val Leu
346 145 150 155 160

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349 Lys Ala Asn Arg Val Trp Gly Ala Leu Arg Gly Leu Glu Thr Phe Ser
350 165 170 175
353 Gln Leu Val Tyr Gln Asp Ser Tyr Gly Thr Phe Thr Ile Asn Glu Ser
354 180 185 190
357 Thr Ile Ile Asp Ser Pro Arg Phe Ser His Arg Gly Ile Leu Ile Asp
358 195 200 205
361 Thr Ser Arg His Tyr Leu Pro Val Lys Ile Ile Leu Lys Thr Leu Asp
362 210 215 220
365 Ala Met Ala Phe Asn Lys Phe Asn Val Leu His Trp His Ile Val Asp
366 225 230 235 240
369 Asp Gln Ser Phe Pro Tyr Gln Ser Ile Thr Phe Pro Glu Leu Ser Asn
370 245 250 255
373 Lys Gly Ser Tyr Ser Leu Ser His Val Tyr Thr Pro Asn Asp Val Arg
374 260 265 270
377 Met Val Ile Glu Tyr Ala Arg Leu Arg Gly Ile Arg Val Leu Pro Glu
378 275 280 285
381 Phe Asp Thr Pro Gly His Thr Leu Ser Trp Gly Lys Gly Gln Lys Asp
382 290 295 300
385 Leu Leu Thr Pro Cys Tyr Ser Arg Gln Asn Lys Leu Asp Ser Phe Gly
386 305 310 315 320
389 Pro Ile Asn Pro Thr Leu Asn Thr Thr Tyr Ser Phe Leu Thr Thr Phe
390 325 330 335
393 Phe Lys Glu Ile Ser Glu Val Phe Pro Asp Gln Phe Ile His Leu Gly
394 340 345 350
397 Gly Asp Glu Val Glu Phe Lys Cys Trp Glu Ser Asn Pro Lys Ile Gln
398 355 360 365
401 Asp Phe Met Arg Gln Lys Gly Phe Gly Thr Asp Phe Lys Lys Leu Glu
402 370 375 380
405 Ser Phe Tyr Ile Gln Lys Val Leu Asp Ile Ile Ala Thr Ile Asn Lys
406 385 390 395 400
409 Gly Ser Ile Val Trp Gln Glu Val Phe Asp Asp Lys Ala Lys Leu Ala
410 405 410 415
413 Pro Gly Thr Ile Val Glu Val Trp Lys Asp Ser Ala Tyr Pro Glu Glu
414 420 425 430
417 Leu Ser Arg Val Thr Ala Ser Gly Phe Pro Val Ile Leu Ser Ala Pro
418 435 440 445
421 Trp Tyr Leu Asp Leu Ile Ser Tyr Gly Gln Asp Trp Arg Lys Tyr Tyr
422 450 455 460
425 Lys Val Glu Pro Leu Asp Phe Gly Gly Thr Gln Lys Gln Lys Leu
426 465 470 475 480
429 Phe Ile Gly Gly Glu Ala Cys Leu Trp Gly Glu Tyr Val Asp Ala Thr
430 485 490 495
433 Asn Leu Thr Pro Arg Leu Trp Pro Arg Ala Ser Ala Val Gly Glu Arg
434 500 505 510
437 Leu Trp Ser Ser Lys Asp Val Arg Asp Met Asp Asp Ala Tyr Asp Arg
438 515 520 525
441 Leu Thr Arg His Arg Cys Arg Met Val Glu Arg Gly Ile Ala Ala Gln
442 530 535 540
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VERIFICATION SUMMARY

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